

SEQUENCE LISTING

<110> Salon et al, John A.

<120> DNA Encoding A Human Melanin Concentrating Hormone Receptor (MCH1) And Uses Thereof

<130> 1795/57453-C/JPW

<140> NotYetKnown

<141> 2001-07-05

<150> 09/610,635

<151> 2000-07-05

<160> 28

<170> PatentIn Ver. 2.1

<210> 1

<211> 1269

<212> DNA

<213> Homo sapiens

<400> 1

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ggtggcaggc gctggaggtt gccgcagcct gcgtgggtgg aggggagctc agctcggtt 180
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ccaaatgcca gcaacaccc tcgtatggcccc gataaacctca cttcagcagg atcacccctt 300
cgcacgggca gcatctccta catcaacatc atcatgcctt cgggtttcgg caccatctgc 360
ctcctggca tcatcgggaa ctccacggtc atcttcgcgg tcgtgaagaa gtccaagctg 420
caactggcaca acaacgtccc cgacatcttc atcatcaacc tctcggtatc agatctcctc 480
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ggggagacca tgcacccctt catcaacggcc atggatgcca atagtcagtt caccagcacc 600
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ggcacctga 1269

<210> 2
<211> 422
<212> PRT
<213> Homo sapiens

<400> 2
Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
405 410 415

Thr Glu Ser Lys Gly Thr
420

<210> 3
<211> 1214
<212> DNA
<213> Rattus norvegicus

<400> 3
gcaggcgacc tgcaccggct gcatggatct gcaaacctcg ttgctgtcca ctggcccaa 60

tgccagcaac atctccgatg gccaggataa tctcacattg ccggggtcac ctccctgcac 120
agggagtgta tcctacatca acatcattat gccttcgtg tttgttacca tctgtctcct 180
gggcacatcgta ggaaactcca cggtcatctt tgctgtggta aagaagtcca agctacactg 240
gtgcagcaac gtcccccaca tcttcatcat caacctctt gtgggtggatc tgctcttcct 300
gctgggcatg ccttcatga tccaccagct catggggaaac ggcgtctggc actttgggaa 360
aaccatgtgc accctcatca cagccatgga cgccaaacagt cagttacta gcacccat 420
cctgactgcc atgaccatgtg accgctactt ggccaccgatc caccatctt cctccacca 480
gttccgaaag ccctccatgg ccaccctggat gatctgcctc ctgtggcgc tctccttcat 540
cagttatcacc cctgtgtggc tctacgcccag gctcattccc ttcccagggg gtgtgtggg 600
ctgtggcata cgcctgccaa accccggacac tgacccatc tgggtactc tgtaccat 660
tttccctggcc tttgccctc cgtttgtggat cattaccgccc gcatacgtga aaatactaca 720
gcccgtacg tcttcgggtt cccacgcctc ccaacgcagc atccggcttc ggacaaagag 780
ggtgacccgc acggccatgtg ccacatgtctt ggtcttctt gtgtgtggg caccctacta 840
tgtgtgcag ctgacccagc tgtccatcag ccggccgacc ctcacgtttt tctacttgta 900
caacgcggcc atcagcttgg gctatgctaa cagctgcctg aaccctttt tgtaatag 960
gctctgtgag acctttcgaa aacgcttggat gttgtcagtg aagcctgcag cccagggca 1020
ctgacaattc cccagtcgccc tccaagtcag gccacccat caaaccgtgg ggagagatac 1140
tgagattaaa cccaggcata ccctgggaga atgcagagggc tggaggctgg gggctttag 1200
caaccacatt ccac 1214

<210> 4

<211> 351

<212> PRT

<213> Rattus norvegicus

<400> 4

Met Asp Leu Gln Thr Ser Leu Leu Ser Thr Gly Pro Asn Ala Ser Asn
1 5 10 15

Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg
20 25 30

Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
35 40 45

Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
100 105 110

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala
130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala
145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
210 215 220

Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala
225 230 235 240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr
325 330 335

Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
340 345 350

Thr

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 5
gggaactcca cggtcatctt cgcggt 26

<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 6
tagcggtcaa tggccatggc ggtcag 26

<210> 7
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 7
ctcctggca tgcccttcat gatccaccag ctcatggca atggg 45

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 8
cttctaggcc tgtacggaag tgtta 25

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 9
gttgtggttt gtccaaactc atcaatg 27

<210> 10
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 10
cgcgatcca ttatgtctgc actccgaagg aaatttg 37

<210> 11
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 11
cgcgaattct tatgtgaagc gatcagagtt cattttc 38

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 12
gcgggatccg ctatggctgg tgattctagg aatg 34

<210> 13
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 13
ccggaattcc cctcacacccg agccctgg 29

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 14
tcagctcggt tgtggagca 20

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<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 15
cttggacttc ttcacgac 18

<210> 16
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: mutated human
MCH1

<400> 16

Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Thr Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
85 90 95

Gly Ser Pro Pro
100

<210> 17

<211> 100

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human
MCH1

<400> 17

Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

Gly Ser Pro Pro
100

<210> 18
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 18
cggcactggc tgggcggacc tggaaggcctc g

31

<210> 19
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 19
cgaggcgttcc aggtccgcggcc agccagtgcc g

31

<210> 20
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 20
atgtcagtgg gagccgcgaa gaagggagtg gg

32

<210> 21
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 21

cccaactccct tcttcgcggc tccccactgac at

32

<210> 22

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 22

taatgtgtct aggtggcgtc agtggggagcc atg

33

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 23

catggctccc actgacgcaca cctagacaca tta

33

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 24

tgacactaag cttcactggc tggatggacc tggaagc

37

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 25

gccccaggaga aagaggagat ctac

24

<210> 26

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human
MCH1

<400> 26

Met	Ser	Val	Gly	Ala	Met	Lys	Lys	Gly	Val	Gly	Arg	Ala	Val	Gly	Leu
1					5				10				15		

Gly	Gly	Gly	Ser	Gly	Cys	Gln	Ala	Thr	Glu	Glu	Asp	Pro	Leu	Pro	Asp
						20			25				30		

Cys	Gly	Ala	Cys	Ala	Pro	Gly	Gln	Gly	Gly	Arg	Arg	Trp	Arg	Leu	Pro
					35			40				45			

Gln	Pro	Ala	Trp	Val	Glu	Gly	Ser	Ser	Ala	Arg	Leu	Trp	Glu	Gln	Ala
	50				55				60						

Thr	Gly	Thr	Gly	Trp	Ala	Asp	Leu	Glu	Ala	Ser	Leu	Leu	Pro	Thr	Gly
65					70				75				80		

Pro	Asn	Ala	Ser	Asn	Thr	Ser	Asp	Gly	Pro	Asp	Asn	Leu	Thr	Ser	Ala
					85				90			95			

Gly	Ser	Pro	Pro	Arg	Thr	Gly	Ser	Ile	Ser	Tyr	Ile	Asn	Ile	Ile	Met
						100			105			110			

Pro	Ser	Val	Phe	Gly	Thr	Ile	Cys	Leu	Leu	Gly	Ile	Ile	Gly	Asn	Ser
						115		120			125				

Thr	Val	Ile	Phe	Ala	Val	Val	Lys	Lys	Ser	Lys	Leu	His	Trp	Cys	Asn
						130		135			140				

Asn	Val	Pro	Asp	Ile	Phe	Ile	Ile	Asn	Leu	Ser	Val	Val	Asp	Leu	Leu
145						150				155			160		

Phe	Leu	Leu	Gly	Met	Pro	Phe	Met	Ile	His	Gln	Leu	Met	Gly	Asn	Gly
						165			170			175			

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
405 410 415

Thr Glu Ser Lys Gly Thr
420

<210> 27
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: mutated human
MCH1

<400> 27

Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
405 410 415

Thr Glu Ser Lys Gly Thr
420

<210> 28

<211> 353

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human
MCH1

<400> 28

Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly Pro Asn Ala Ser Asn
1 5 10 15

Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg
20 25 30

Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
35 40 45

Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala
50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile
65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
100 105 110

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala
130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala
145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile

210	215	220
Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val Ala		
225	230	235
240		
Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg		
245	250	255
Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr		
260	265	270
Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr		
275	280	285
Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser		
290	295	300
Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys		
305	310	315
320		
Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala		
325	330	335
Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly		
340	345	350

Thr